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"Systems Biology of
Macrophages"

Date: Wednesday,
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Time: 1:00-2:00 EST
Location: Clark Hall 110
Simulcast to Talbot
Library

Abstract:

Cells and tissues function in context. Under a given growth or survival medium they perform tasks, replicate and die. Given a stimulus they respond by invoking myriad biomolecular networks that result in a specified cellular outcome. At any given instant it can be argued that the cell is in a "state" defined by its components – their concentrations and locations, the interactions between components – that are modulated in space and time, and the complex circuitry – that involves a large number of interacting networks and a snapshot of the dynamical processes – such as gene expression, cell cycle, transport of components, etc. At present, we can measure, using high and low throughput methods, several cellular components in a context-dependent manner and obtain a partial picture of cellular networks and dynamical processes. Are these measurements sufficient to answer important biological questions and help reconstruct a systems-level of understanding of a mammalian cell? This talk will address strategies developed to address this question and demonstrate the power of integration of diverse cellular data for answering interesting biological questions in macrophages. We will use this systems biology approach to address the following questions:

- How good are macrophage cell lines in addressing phenotypic biology of primary macrophages?
- How can we combine proteomic and other cellular measurements to characterize the repertoire of upstream signaling networks invoked by macrophages?
- How do signals associated with inflammatory molecules regulate gene transcription in macrophages?
- How does lipid signaling influence the proteomic pathways associated with Toll receptor pathways?
- How can we combine heterogeneous data to quantitatively decipher cross-talk in macrophage signaling?
- How do designed knockdowns of proteins influence cellular phenotypes?